International Journal of Agricultural Science and Research (IJASR)
ISSN (P): 2250-0057; ISSN (E): 2321-0087
Vol. 7, Issue 5, Oct 2017, 265-270

PRINCIPAL COMPONENT ANALYSIS OF MORPHOLOGICAL AND YIELD ATTRIBUTING TRAITS IN ADVANCED BREEDING LINES OF RICE GROWN AT RAINFED SHALLOW LOWLAND CONDITION OF WEST BENGAL

VANGARU SATHISH[1] & B. K. SENAPATI[2]

[1]*Department of Genetics, Krishi Viswavidyalaya, Mohanpur, West Bengal, India*

[2]*Plant Breeding, Bidhan Chandra, Krishi Viswavidyalaya, Mohanpur, West Bengal, India*

ABSTRACT

The current investigation was carried out used in the study comprising of high yielding advanced breeding lines collected from IVT-RSL, RRSS-Chakdah, Nadia, in a field experiment using a randomized block design with two replications to determine the relationship and genetic diversity among 49 rice germplasm accessions, using principal component analysis for rain fed shallow lowland condition. Observations were taken for Various morphological and yields and its attributing traits. In this study, Component-1 had the contribution from the traits viz., grain L/B ratio, grain length and harvest index which accounted 25.5 % of the total variance. Seed yield per plant, panicle weight, number of grains/panicle and number of florets/panicles have contributed 15.35 % of the total variability in component-2. No of secondary branches/panicle, days to 50% flowering and days to maturity contributed 12.97 % variability towards component-3. 1000-grain weight and grain breadth contributed 10.84% variation towards component-4. In principle component-5, characters plant height and panicle length together contributed 7.91% variability. The cumulative variance of 72.58 % of total variation among 20 characters was explained by the first five components. Thus the results of principal component analysis revealed wide genetic variability exists in this rice germplasm accessions.

***KEYWORDS**: Rice, Variability and Principle Component Analysis*

Received: Aug 10, 2017; **Accepted**: Aug 30, 2017; **Published**: Sep 23, 2017; **Paper Id**.: IJASROCT201732

Original Article

INTRODUCTION

Rice (Oryza sativa L.) is one of the most extensively cultivated cereal crops in the world, spreading across a wide range of geographies, ecological and climatic regions (Surapaneni *et al.,* 2016). Rice is the life and the prince among cereals as this unique grain helps to sustain two thirds of the world's population. Rice is being the staple food for more than 70 percent of our national population along with the source of livelihood for 120-150 million rural households. It is a backbone to the Indian agriculture. Multivariate analysis is a method of statistics used to summarize and describing the inherent variation present in population of crop genotypes. Multivariate analysis two types viz., Principal component analysis (PCA) and Cluster analysis and discriminate analysis (Oyelola, 2004), the former one is used to uncover similarities between variables and classify the genotypes while cluster analysis on the other hand is concerned with classifying previously unclassified materials (Leonard and Peter, 2009). The current study was done to identify and classify variation for grouping the accessions of rice by taking several characters and relationship into account.

MATERIALS AND METHODS

In this study, 49 Rice cultivars were raised under rain-fed shallow low land condition. The experiment was conducted during Aman (Karif) season of 2014 at the Regional Research Sub Station, Bidhan Chandra Krishi Viswavidyalya, Chakdah, and Nadia. The experimental field is situated at 23o-30’ N, longitude 89” E and altitude 9.75 m (above mean sea level) in the New Alluvial Zone of West Bengal, India. The experiment was laid out in Randomized block design with two replications; the plot had size of 5 × 3m. A spacing of 60 cm between plots, 20 cm between rows and 15 cm between plants was maintained. Recommended cultural practices have been applied in order to get a good harvest. Five plants were selected randomly from each genotype in each replication to record the yield and its attributing characters viz., Days to 50% flowering Days to maturity, Plant height (cm), No. of panicles per plant, Panicle weight (g), Panicle length (cm), No. of primary branches per panicle, No. of secondary branches per panicle, Number of florets per panicle, Number of grains per panicle, Floret fertility (%), 1000 grain weight (g), Grain length (mm), Grain breadth (mm), Grain l/b ratio (mm), Kernel length (mm), Kernel breadth (mm), Kernel l/b ratio, Harvest index (%) and Seed Yield/plant (g).

The principal component analysis method explained by Harman (1976) was followed in the extraction of the components. The percentage variances explained by each component were determined (Harman, 1976; Sharma, 1996; Tadesse and Bekele, 2001). Principal component analysis, loading plot (Figure 1) and biplot (Figure 2) graphical display were performed using XLSTAT Version 2014.5.03 software for all the traits of rice cultivars.

RESULTS AND DISCUSSIONS

Principal component analysis has shown the genetic diversity of the germplasm lines and cumulative variance of 72.58 % (Table No.01) explained by the first five axes with an Eigen value of greater than unity indicates that, the identified traits within the axes exhibited great influence on the phenotype of germplasm lines. All the genotypes were widely scattered across different quarters (Figure 2). In this study, we chose to follow the criterion used by Clifford and Stephenson (1975) and corroborated by Guei *et al.* (2005), which suggested that, the first three principal components are often the most important in reflecting the variation patterns among accessions, and the characters associated with these are more useful in differentiating accessions. According to this criterion, the first three components account for more than 53.82 % of total variation, giving a clear idea of the structure underlying the variables analyzed. PCA has been used in rice by Vishnu *et al.* (2014), Ravi Kumar *et al. (*2015) and Gour *et al.* (2017) for partitioning observed variation and classifying the genotypes in a population based on prominent traits.

The first principal component accounted for 25.49 % of the total variation in the population (Table-1). Kernel L/B ratio contributed more to the variation followed by a grain L/B ratio. Characters like No of panicles per plant, Kernel breadth and Harvest index contributed negatively to the first component. Second principal component contributed 15.35 % of the total variation. Characters that contributed to the component include panicle weight, number of grains per panicle and number of florets per panicle. Characters like Number of secondary branches per panicle, days to 50% flowering, days to maturity and floret fertility contributed 12.97 variations towards third principal component. In this principal component, floret fertility contributed negatively. The fourth principal component accounted for 10.85 % of the total variation in the population. 1000 grain weight contributed more to the variation, followed by grain breadth and No. of primary branches per panicle in principal component 4. The fifth principal component accounted for 7.91 % of the total variation with panicle length given the highest contribution. Cumulatively, these first five principal components explained 72.58 % of the

total variation in the population. Thus, important characters coming together in different principal components and contributing towards explaining the variability and have the tendency to stay together (Mahendran *et al*., 2013) and offer opportunity for utilizing in crop improvement programs.

CONCLUSIONS

Principal component analysis, classified the variation existing in germplasm studied, based on the identified prominent characters like grain L/B ratio, grain length, harvest index seed yield per plant, panicle weight, number of grains/panicle and number of florets/panicles, No of secondary branches/panicle, days to 50% flowering and days to maturity, 1000-grain weight and panicle length. Thus the principal component analysis was helpful, in revealing the high level of genetic variation existing in the population and explains, which characters contribute for genetic diversity among the genotypes in the population. This will make opportunity for further improvement of the cultivars, in breeding programs by helping with selection of parents suitable for morphological traits, analyzed in this study.

REFERENCES

1. *Aliyu, B., Akoroda, M.O., & Padulosi, S. (2000). Variation within Vigna reticulate Hooke FII. Nigerian journal of genetics. pp. 1-8.*
2. *Ariyo, Q.J., & Odulaja, A. (1991). Numerical analysis of variation among accessions of Okra (Abelmoschus esculentus). Annals of Botany, 67, 527–31.*
3. *Clifford, H.T., & Stephenson, W. (1975). An Introduction to Numerical Classification. Academic Press, London, pp. 229.*
4. *Gour, L., Maurya, S.B., Koutu, G.K., Singh, S.K., Shukla, S.S., & Mishra, D.K. (2017). Characterization of rice (Oryza sativa L.) genotypes using principal component analysis, including scree plot & rotated component matrix. International Journal of Chemical Studies, 5 (4): 975-983.*
5. *Guei, R.G., Sanni, K. A., & Fawole, A.F.J. (2005). Genetic diversity of rice (Oryza sativa). Agronomy Africaine, 5:17–28.*
6. *Harman, H.H. (1976). Modern factor analysis. 3nd Ed. University of Chicago Press, Chicago, pp. 376.*
7. *Leonard, K. & Peter, R.J. (2009). Finding Groups in Data: An Introduction to Cluster Analysis. Pp. 344.*
8. *Mahendran, P., Veerabadhiran, P., Robin, S., & Raveendran, M. (2015). Principal component analysis of rice germplasm accessions under high temperature stress. International Journal of Agricultural Science and Research, 5 (3): 355-360.*
9. *Oyelola, B.A. (2004). The Nigerian Statistical Association preconference workshop. Pp. 20-21. University of Ibadan.*
10. *Ravikumar, B.N.V.S.R., NagaLumari, P., Rao, V. R. M. P., Girija, R. P.V., Satyanarayana, N., Chamundeswari, K., Mohan V., Suryanarayana, Y., Bharathalakshmi, M., & Reddy, A.V. (2015). Principal component analysis and character association for yield components in rice (Oryza sativa L.) cultivars suitable for irrigated ecosystem. Current Biotica, 9 (1): 25-35.*
11. *Sharma, S. (1996). Applied multivariate techniques. IInd Ed. John Wiley and Sons, New York, pp-493.*
12. *Surapaneni, M., Divya B., Sukumar, M., Raju A.K., Rao, V.Y., & Neelamraju. S. (2016). Genetic characterization and population structure of Indian rice cultivars and wild genotypes using a core set markers. 3 Biotech, 6:95.*
13. *Tadesse, W., & Bekele, E. (2001). Factor analysis of yield in grasspea (Lathyrus sativus L.). Lathyrus Lathyrism Newsletter, 2: 416-421.*
14. *Vishnu, V.N., Robin S., Sudhakar, D., Raveendran, M., Rajeswari, S. And Manonmani, S. (2014). Evaluation of Rice Genetic Diversity and Variability in a Population Panel by Principal Component Analysis. Indian Journal of Science and Technology,*

7 (10), 1555–1562.

APPENDICES

Table 1: Eigen Value, Factor Scores and Contribution of the First Five Principal Component Axes to Variation in Rice Varieties

Parameter	PC-1	PC-2	PC-3	PC-4	PC-5
Eigenvalue	5.098	3.071	2.595	2.169	1.584
Variability (%)	25.492	15.355	12.977	10.845	7.918
Cumulative %	25.492	40.847	53.825	64.669	72.587
Days to 50 % flowering	0.431	-0.115	0.567	-0.306	-0.335
Days to maturity	0.420	-0.104	0.548	-0.421	-0.373
Plant height at maturity	0.383	0.033	-0.240	0.269	-0.438
No of panicles per plant	-0.443	0.242	-0.356	-0.280	0.257
Panicle weight	0.257	0.757	0.028	0.273	-0.291
Panicle length	0.376	0.346	0.362	0.130	0.539
No. of primary branches per panicle	0.148	-0.053	0.270	0.443	0.405
No. of secondary branches per panicle	0.350	0.045	0.612	0.135	0.446
Number of florets per panicle	0.148	0.644	0.419	-0.344	0.024
Number of grains per panicle	-0.084	0.733	0.175	-0.448	-0.120
Floret fertility (%)	-0.267	0.248	-0.486	-0.164	-0.143
1000 grain weight	0.206	0.294	-0.326	0.726	-0.187
Grain length	0.859	0.265	-0.117	0.134	0.013
Grain breadth	-0.465	0.163	0.430	0.517	-0.095
Grain l/b ratio	0.865	0.049	-0.348	-0.221	0.051
Kernel length	0.843	0.302	-0.057	0.243	-0.057
Kernel breadth	-0.590	0.264	0.417	0.375	-0.314
Kernel l/b ratio	0.878	-0.041	-0.311	-0.072	0.211
Harvest index	-0.583	0.499	-0.144	-0.069	0.326
Seed Yield/plant	-0.168	0.825	-0.219	-0.154	0.034

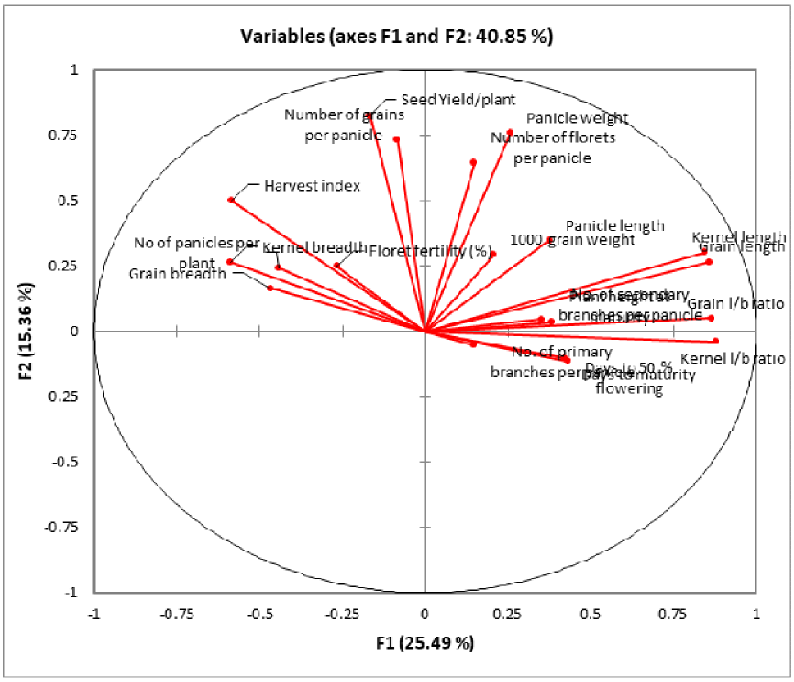

Figure 1: Loading Plot of Various Traits in Rice Germplasms

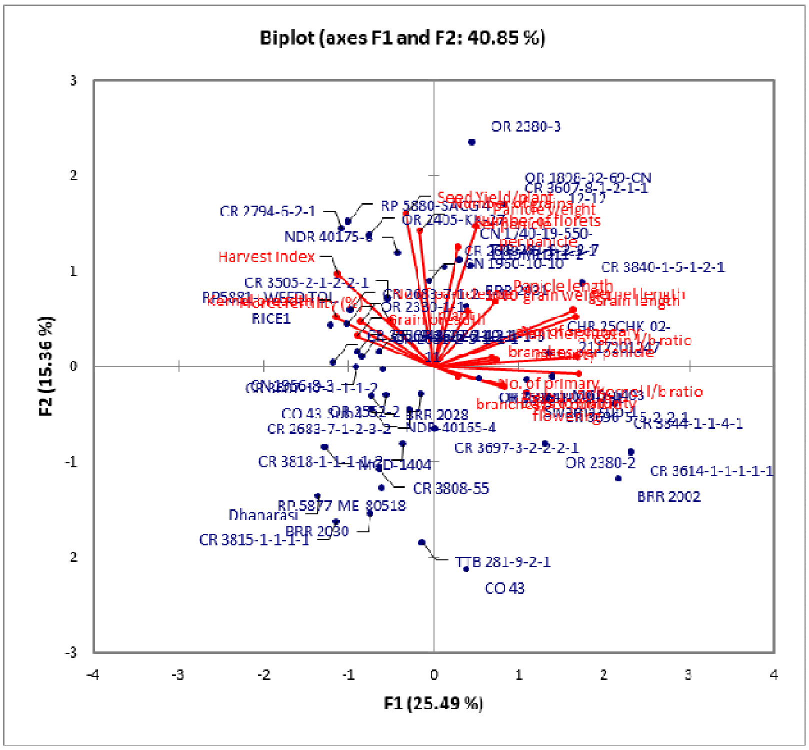

Figure 2: Distribution of Genotypes across Two Components